

SEQUENCE LISTING



192

288

<110> Bertin, John Wang, Weive Blatcher, Maria

<120> NOVEL MOLECULES OF THE NBS/LRR PROTEIN FAMILY AND USES THEREOF

<130> 07334-333001

<140> US 09/986,224

2001-10-22

<150> US 09/848,035 <151> 2001-05-03

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20

ccc ctc gaa gac gtg cta cag aag acc cca tgg tct gag gtg gaa gag Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu 35 40

get gat gge aag aaa etg gea gaa att etg gte aac ace tee tea gaa Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu 50 55

aat tgg ata agg aat gcg act gtg aac atc ttg gaa gag atg aat ctc 240 Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu 65 70

acg gaa ttg tgt aag atg gca aag gct gag atg atg gag gac gga cag Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln 85 90

		aat Asn					tcg Ser	336
							gag Glu	384
		tgg Trp						432
		gtc Val 150						480
		ccc Pro						528
		gtg Val						576
		tgc Cys						624
		gag Glu						672
		gac Asp 230						720
		cag Gln						768
		cct Pro						816
		ccg Pro						864
		agg Arg						912
		cag Gln 310						960

gt: Va	g gaç l Glu	9 99 1 Gl	c tto y Phe	cts Leu 325	ı Glı	gag ıGlu	ga Asi	agg Arg	g agg g Arg 330	g Ala	tai a Tyi	t tto	e cto	aga Arc	cac His	1008
Phe	gga Gly	ga Ası	gag Glu 340	ı Asp	caa Glr	geo Ala	ato Met	egt Arg 345	Ala	ttt Phe	gag Glu	g cta 1 Lei	ato Met	Arg	agc Ser	1056
Asr	gcg Ala	355	ctg Leu	Phe	cag Gln	ctg Leu	360 GJ ^A GGG	Ser	geo Ala	Pro	geg Ala	gtg Val 365	Cys	tgg	att	1104
gtg Val	Cys 370	Thi	act Thr	ctg Leu	a ag Lys	ctg Leu 375	cag Gln	atg Met	gag Glu	aag Lys	380 380	Glu	gac	ccg Pro	ccg Pro	1152
Val 385	Pro	Ala	ggg	Arg	Thr 390	Ala	Ala	Gly	Arg	Ala 395	Ala	Asp	Ala	Glu	Pro 400	1200
Pro	Gly	Arg	gca Ala	Gly 405	Leu	Trp	Ala	Gln	Met 410	Ser	Val	Phe	His	Arg 415	Glu	1248
Asp	Leu	Glu	agg Arg 420	Leu	Gly	Val	Gln	Glu 425	Ser	Asp	Leu	Arg	Leu 430	Phe	Leu	1296
Asp	Gly	Asp 435	atc Ile	Leu	Arg	Gln	Asp 440	Arg	Val	Ser	Lys	Gly 445	Cys	Tyr	Ser	1344
Phe	Ile 450	His	ct c Leu	Ser	Phe	Gln 455	Gln	Phe	Leu	Thr	Ala 460	Leu	Phe	Tyr	Ala	1392
Leu 465	Glu	Lys	gag Glu	Glu	Glu 470	Glu	Asp	Arg	Asp	Gly 475	His	Ala	Trp	Asp	Ile 480	1440
Gly	Asp	Val	cag Gln	Lys 485	Leu	Leu	Ser	Gly	Glu 490	Glu	Arg	Leu	Lys	Asn 495	Pro	1488
Asp	Leu	Ile	caa Gln 500	Val	Gly	His	Phe	Leu 505	Phe	Gly	Leu	Ala	Asn 510	Glu	Lys	1536
Arg	Ala	Lys 515	gag Glu	Leu	Glu	Ala	Thr 520	Phe	Gly	Cys	Arg	Met 525	Ser	Pro	Asp	1584
Ile	aaa Lys 530	cag Gln	gaa Glu	ttg Leu	Leu	caa Gln 535	tgc Cys	aaa Lys	gca Ala	His	ctt Leu 540	cat His	gca Ala	aat Asn	aag Lys	1632

				a ag Lys					1680
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				cac His					2112
				aga Arg					2160
				gcc Ala					2208
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aca cqc cca aaa cac ttc ctg cag atg ttg tcg ttg gaa aac tgt cgt Thr Arg Pro Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg ctt aca qaa qcc aqt tgc aag gac ctt gct gct gtc ttg gtt gtc agc

Leu Thr Glu Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser aag aag ctg aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca Lys Lys Leu Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr

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<213> Homo sapiens

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Trp Glu Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg Ala Leu Arg Asp Leu Gln Leu Leu Ala Gln Gln Pro Ile Tyr Ile Arg Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Ala Leu Glu Lys Glu Glu Glu Asp Arg Asp Gly His Ala Trp Asp Ile Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn Pro Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu Lys Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp Ile Lys Gln Glu Leu Leu Gln Cys Lys Ala His Leu His Ala Asn Lys Pro Leu Ser Val Thr Asp Leu Lys Glu Val Leu Gly Cys Leu Tyr Glu Ser Gln Glu Glu Glu Leu Ala Lys Val Val Val Ala Pro Phe Lys Glu Ile Ser Ile His Leu Thr Asn Thr Ser Glu Val Met His Cys Ser Phe Ser Leu Lys His Cys Gln Asp Leu Gln Lys Leu Ser Leu Gln Val Ala Lys Gly Val Phe Leu Glu Asn Tyr Met Asp Phe Glu Leu Asp Ile Glu Phe Glu Ser Ser Asn Ser Asn Leu Lys Phe Leu Glu Val Lys Gln Ser Phe Leu Ser Asp Ser Ser Val Arg Ile Leu Cys Asp His Val Thr Arg Ser Thr Cys His Leu Gln Lys Val Glu Ile Lys Asn Val Thr Pro Asp Thr Ala Tyr Arg Asp Phe Cys Leu Ala Phe Ile Gly Lys Lys Thr Leu Thr His Leu Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met Leu Met Leu Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr

Leu Arg Leu Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe 725 730 Phe Tyr Val Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser 745 Ala Asn Val Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met 760 765 Thr Arg Pro Lys Wis Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg 775 780 Leu Thr Glu Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser 790 795 Lys Lys Leu Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr 805 810 Gly Val Lys Phe Leu 820 <210> 3 <211> 1895 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)...(1893) atg gca gaa teg gat tet act gac ttt gac etg etg tgg tat eta gag 4.8 Met Ala Glu Ser Asp Ser Thr Asp Phe Asp Leu Leu Trp Tyr Leu Glu aat ctc agt gac aag gaa ttt cag agt ttt aag aag tat ctg gca cgc 96 Asn Leu Ser Asp Lys Glu Phe Gln Ser Phe Lys Lys Tyr Leu Ala Arg aag att ctt gat ttc aaa ctg cca cag ttt cca ctg ata cag atg aca 144 Lys Ile Leu Asp Phe Lys Leu Pro Gln Phe Pro Leu Ile Gln Met Thr 40 aaa gaa gaa ctg gct aac gtg ttg cca atc tct tat qaq qqa caq tat 192 Lys Glu Glu Leu Ala Asn Val Leu Pro Ile Ser Tyr Glu Gly Gln Tyr 55 ata tgg aat atg ctc ttc agc ata ttt tca atg atg cgt aag gaa gat 240 Ile Trp Asn Met Leu Phe Ser Ile Phe Ser Met Met Arg Lys Glu Asp ctt tgt agg aag atc att ggc aga cga aac cat gtg ttc tac ata ctt 288 Leu Cys Arg Lys Ile Ile Gly Arg Arg Asn His Val Phe Tyr Ile Leu caa tta gcc tat gat tct acc agc tat tat tca gca aac aat ctc aat 336 Gln Leu Ala Tyr Asp Ser Thr Ser Tyr Tyr Ser Ala Asn Asn Leu Asn 105 gtg ttc ctg atg gga gag aga gca tct gga aaa act att qtt ata aat 384 Val Phe Leu Met Gly Glu Arg Ala Ser Gly Lys Thr Ile Val Ile Asn

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	Tyr		gtt Val			Thr					Asn				aac Asn 160	480
			gct Ala							Trp					Ala	528
			gac Asp 180													576
			gac Asp													624
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agt Ser 225	ttg Leu	ctg Leu	aag Lys	aga Arg	aaa Lys 230	atg Met	gct Ala	cca Pro	ggc Gly	tgc Cys 235	tgg Trp	ttc Phe	ctc Leu	atc Ile	tcc Ser 240	720
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gat Asp	tgc Cys	tgc Cys	acg Thr 260	acc Thr	ttg Leu	cag Gln	ctg Leu	teg Ser 265	aat Asn	Gly 999	aag Lys	agg Arg	gag Glu 270	ata Ile	tat Tyr	816
ttt Phe	aac Asn	tct Ser 275	ttc Phe	ttt Phe	aaa Lys	gac Asp	ege Arg 280	cag Gln	agg Arg	gcg Ala	tcg Ser	gca Ala 285	gcc Ala	ctc Leu	cag Gln	864
			gag Glu		Glu											912
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cgt Arg	gac Asp	ttc Phe	cag Gln	ctc Leu 325	tgc Cys	tgc Cys	caa Gln	Thr	ccc Pro 330	act Thr	gat Asp	cta Leu	cat His	gcc Ala 335	cac His	1008
Phe	ctt Leu	gct Ala	gat Asp 340	gcg Ala	ttg Leu	aca Thr	Ser	gag Glu 345	gct Ala	gga Gly	ctt Leu	act Thr	gcc Ala 350	aat Asn	cag Gln	1056

cac His								1104
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ttt Phe								1200
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cag Gln								1296
ctg Leu								1344
tct Ser 450								1392
aac Asn								1440
gta Val								1488
cgt Arg								1536
tat Tyr								1584
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tta Leu								1680
gtt Val								1728

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235

 Ser Arg Pro Thr Arg Gly Asn Asn Val Lys Thr Phe Leu Lys Glu Val
 245
 250
 255

 Asp Cys Cys Thr Thr Leu Gln Leu Ser Asn Gly Lys Arg Glu Tile Tyr

 260
 265
 270

Phe Asn Ser Phe Phe Lys Asp Arg Gln Arg Ala Ser Ala Ala Leu Gln Leu Val His Glu Asp Glu Ile Leu Val Gly Leu Cys Arg Val Ala Ile Leu Cys Trp Ile Thr Cys Thr Val Leu Lys Arg Gln Met Asp Lys Gly Arg Asp Phe Gln Leu Cys Cys Gln Thr Pro Thr Asp Leu His Ala His Phe Leu Ala Asp Ala Leu Thr Ser Glu Ala Gly Leu Thr Ala Asn Gln Tyr His Leu Gly Leu Leu Lys Arg Leu Cys Leu Leu Ala Ala Gly Gly Leu Phe Leu Ser Thr Leu Asn Phe Ser Gly Glu Asp Leu Arg Cys Val Gly Phe Thr Glu Ala Asp Val Ser Val Leu Gln Ala Ala Asn Ile Leu Leu Pro Ser Asn Thr His Lys Asp Arg Tyr Lys Phe Ile His Leu Asn Val Gln Glu Phe Cys Thr Ala Ile Ala Phe Leu Met Ala Val Pro Asn Tyr Leu Ile Pro Ser Gly Ser Arg Glu Tyr Lys Glu Lys Arg Glu Gln Tyr Ser Asp Phe Asn Gln Val Phe Thr Phe Ile Phe Gly Leu Leu Asn Ala Asn Arg Arg Lys Ile Leu Glu Thr Ser Phe Gly Tyr Gln Leu Pro Met Val Asp Ser Phe Lys Trp Tyr Ser Val Gly Tyr Met Lys His Leu Asp Arg Asp Pro Glu Lys Leu Thr His His Met Pro Leu Phe Tyr Cys Leu Tyr Glu Asn Arg Glu Glu Glu Phe Val Lys Thr Ile Val Asp Ala Leu Met Glu Val Thr Val Tyr Leu Gln Ser Asp Lys Asp Met Met Val Ser Leu Tyr Cys Leu Asp Tyr Cys Cys His Leu Arg Thr Leu Lys Leu Ser Val Gln Arg Ile Phe Gln Asn Lys Glu Pro Leu Ile Arg Pro Thr Ala Ser Gln Met Lys Ser Leu Val Tyr Trp Arg Glu Ile Cys Ser Leu Phe Tyr Thr Met Glu Ser Leu Arg Glu Leu His Ile Phe Asp Asn Asp Leu Asn Gly Ile Ser Glu Arg Ile Leu Ser Lys Ala Leu Glu His Ser Ser Cys Lys Leu Arg Thr Leu

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<220> <221> CDS

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cag Gln	cgc Arg	cta Leu 35	ctg Leu	gat Asp	cct Pro	aat Asn	agg Arg 40	act Thr	aga Arg	gcc Ala	cag Gln	gcc Ala 45	cag Gln	acg Thr	ata Ile	1	.44
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acc Thr	ttt Phe	gct Ala	gaa Glu 100	ttg Leu	att Ile	tct Ser	ttg Leu	gat Asp 105	tgg Trp	ccc Pro	gat Asp	ttt Phe	gat Asp 110	gcc Ala	ccc Pro	3	36
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gat Asp 145	ggc Gly	tcg Ser	cca Pro	tgt Cys	aca Thr 150	gac Asp	tgg Trp	tac Tyr	cag Gln	gag Glu 155	ctc Leu	cca Pro	gtg Val	acc Thr	aaa Lys 160	4	180
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		cag Gln														720
		atg Met														768
		tat Tyr														816
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Asp	His	Val	Tyr 20	Ile	Arg	Asn	Thr	Ser 25		Asp	Glu	His	Glu 30	Glu	Leu	
Gln	Arg	Leu 35	Leu	Asp	Pro	Asn	Arg 40	Thr	Arg	Ala	Gln	Ala 45	Gln	Thr	Ile	
Val	Leu 50		Gly	Arg	Ala	Gly 55		Gly	Lys	Thr	Thr		Ala	Met	Gln	
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Tyr	Val	Phe	Tyr	Leu		Cys	His	Lys			Tyr	Met	Lys	Glu		
Thr	Phe	Δla	Glu	85 Leu	Tle	Ser	Leu	Asp	90 Trp	Pro	Asp	Phe	Asp	95 Ala	Pro	
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		115				Gln	120					125				
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		Ser	Pro	Cys		Asp	Trp	Tyr	Gln		Leu	Pro	Val	Thr	Lys	
145	T	TI é o	C 0 2	T 011	150	Lys	Tire	Glu	T. 011	155 Val	Dro	T.011	Δla	Thr	160 Leu	
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Leu	Ile	Thr	11e 180	Lys	Thr	Trp	Phe	Val 185	Arg	Asp	Leu	Lys	Ala 190	Ser	Leu	
Val	Asn	Pro		Phe	Val	Gln	11e 200		Gly	Phe	Thr	Gly 205	Asp	Asp	Leu	
Arg	Val 210		Phe	Met	Arg	His 215		Asp	Asp	Ser	Ser 220	Glu	Val	Glu	Lys	
Ile		Gln	Gln	Leu	Arg	Lys	Asn	Glu	Thr	Leu		His	Ser	Cys	Ser	
225					230					235					240	

Ala Pro Met Val Cys Trp Thr Val Cys Ser Cys Leu Lys Gln Pro Lys 250 245 Val Arg Tyr Tyr Asp Leu Gln Ser Ile Thr Gln Thr Thr Thr Ser Leu 260 265 Tyr Ala Tyr Phe Phe Ser Asn Leu Phe Ser Thr Ala Glu Val Asp Leu 275 285 280 Ala Asp Asp Ser Trp Pro Gly Gln Trp Arg Ala Leu Cys Ser Leu Ala 300 295 Ile Glu Gly Leu Trp Ser Met Asn Phe Thr Phe Asn Lys Glu Asp Thr 315 310 Glu Ile Glu Gly Leu Glu Val Pro Phe Ile Asp Ser Leu Tyr Glu Phe 325 330 Asn Ile Leu Gln Lys Ile Asn Asp Cys Gly Gly Cys Thr Thr Phe Thr 340 345 His Leu Ser Phe Gln Glu Phe Phe Ala Ala Met Ser Phe Val Leu Glu 355 360 365 Glu Pro Arg Glu Phe Pro Pro His Ser Thr Lys Pro Gln Glu Met Lys 375 380 Met Leu Leu Gln His Val Leu Leu Asp Lys Glu Ala Tyr Trp Thr Pro 390 395 Val Val Leu Phe Phe Phe Gly Leu Leu Asn Lys Asn Ile Ala Arg Glu 405 410 Leu Glu Asp Thr Leu His Cys Lys Ile Ser Pro Arg Val Met Glu Glu 425 Leu Leu Lys Trp Gly Glu Glu Leu Gly Lys Ala Glu Ser Ala Ser Leu 440 445 435 Gln Phe His Ile Leu Arg Leu Phe His Cys Leu His Glu Ser Gln Glu 455 460 Glu Asp Phe Thr Lys Lys Met Leu Gly Arg Ile Phe Glu Val Asp Leu 470 475 Asn Ile Leu Glu Asp Glu Glu Leu Gln Ala Ser Ser Phe Cys Leu Lys 485 490 495 His Cys Lys Arg Leu Asn Lys Leu Arg Leu Ser Val Ser Ser His Ile 500 505 Leu Glu Arg Asp Leu Glu Ile Leu Glu 515

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<220> <221> CDS <222> (2)...(2575)

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310

325

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